34. The method as claimed in claim 33, wherein the oligoners are labeled with ^{32}P.

35. The method as claimed in claim 26, wherein the oligonucleotides have a length of from 8 to 20 nucleotides.

36. The method as claimed in claim 26, wherein the oligonucleotides are attached to the surface as an array of a parallel stripes, and at least two polynucleotides are analyzed simultaneously by applying the polynucleotides to the array in the form of separate stripes orthogonal to the oligonucleotide stripes.

37. The method as claimed in claim 26 wherein hybridization is effected in the presence of tetramethylammonium chloride at a concentration of 1M to 5M.--

Claim 21, cancel without prejudice to the subject matter thereof and add the following claim in its place.

--38. The method of claim 19, where the size of each discrete cell is between an average size of 10 and 100 microns.--

Claim 24, cancel without prejudice to the subject matter thereof and add the following claim in its place.

--39. Apparatus for analyzing a polynucleotide, the apparatus comprising a support segregated into at least two cells, each cell having attached thereto oligonucleotides of defined sequence, where the defined sequence of the oligonucleotides of a first cell is different from the defined sequence of the oligonucleotides of a second cell.--

REMARKS

Favorable reconsideration is respectfully requested.

The claims are 17 to 20, 22, 23 and 25 to 39.

The allowance of claims 17 to 20, 22 and 23 is

acknowledged with appreciation. However, for reasons discussed below, it is considered that all of the claims in this application are now in condition for allowance.

At this point, applicants also wish to acknowledge the helpful telephone interview with Examiner Marschel in which the indefiniteness issue was discussed. While no formal agreements were reached at said interview, it is believed that the present claims recite an apparatus and method substantially along the lines which the Examiner had indicated might be acceptable.

In this regard, the term "chosen" was criticized in the previous claims and the present claims do not recite such term, but instead recite "defined" i.e. "defined lengths" rather than "chosen lengths".

With regard to the rejection of the term "defined", such term continues to be employed in the present claims since anyone would know whether a particular sequence was defined or undefined.

With regard to support for the present claims, new claims 25 and 26 are based on previous claims 1, 2, 8 and 9.

New claims 28 to 37 are based on previous claims 4 to 7 and 11 to 16, respectively.

New claims 38 and 39 are based on previous claims 21 and 24, respectively.

The alleged indefiniteness in previous claim 21 is now clarified by the above amendment i.e. in new claim 38.

Turning to the rejection on prior art, it is noted that previous claims 5, 7, 12 to 16 and 21 are stated to be allowable over the prior art. Accordingly, the corresponding claims, namely, 29, 31, 33 to 37 and 39, are likewise considered to be allowable over the prior art.

New claims 25 and 26 differ from allowed apparatus claims 17 and 18 in that there is no requirement for covalently binding the oligonucleotides to the solid support and there is no

requirement for the oligonucleotide of one cell to be different from the oligonucleotide of another cell.

Claims 1 to 3, 6, 8 to 10 and 24 have been rejected under 35 U.S.C. 102(b) as being clearly anticipated by Brigati et al. and claims 1 to 4 and 8 to 11 have been rejected under 35 U.S.C. 102(b) as being clearly anticipated by Saiki et al.

These rejections are respectfully traversed.

Neither the Brigati et al. reference nor the Saiki et al. reference teach solid supports having attached oligonucleotides of "defined sequences".

The Saiki et al. reference involves applying PCR amplified DNA samples of given lengths to nylon filters. However, there is nothing in this reference which teaches or suggests that the sequence of the amplified DNA samples is defined. Indeed, the amplified DNA samples of Saiki et al. are not defined because they are being applied to the nylon solid support for the purpose of detecting the presence or absence of certain bases.

Thus, the apparatus of the present claims includes a support having oligonucleotides attached to a support surface. The oligonucleotides have defined sequences with different oligonucleotides having different lengths or sequences.

Similarly, Applicant's claimed method involves applying unknown polynucleotides to a support having attached oligonucleotides of defined sequence and detecting whether or note the polynucleotides hybridize to the attached oligonucleotides (reverse dot blot method).

In contrast to Applicant's apparatus employing a support with attached oligonucleotides of defined sequences and Applicant's reverse dot blot method, the Saiki et al. reference discloses nylon supports having attached PCR amplified products of unknown sequence. The nylon supports with attached unknown DNA are exposed to synthesized allele specific (ASO) probes of known DNA sequences in a normal dot blot diagnostic method.

There is nothing in the Saiki et al. reference which teaches or suggests supports having attached oligonucleotides of defined sequences.

Again, the amplified DNA samples of Saiki et al. are not defined because they are being applied to the nylon support for the purpose of detecting the presence or absence of certain bases.

Similarly, the Brigati et al. reference relates to solid support attached viral DNA samples which are defined only in terms of their source. The reference gives no indication that the actual sequence of the viral DNA is defined and in fact it can only be concluded that the DNA sequence is not defined, for the same reasons stated for the Saiki et al. reference.

The Brigati et al. reference is similar to the Saiki et al. reference in that unknown genomic DNA is attached to a support and known viral specific probes are used to probed the genomic DNA. The Brigati et al. reference gives no indication that the actual sequence of the viral DNA is defined and in fact it can be concluded only that the DNA sequence is not defined because it is being probed with DNA probes for the purpose of detecting the presence of specific genomes. Thus, like the Saiki et al. reference the Brigati et al. reference does not teach or suggest supports having attached oligonucleotides of defined sequences.

Additionally, the Brigati et al. reference does not teach or suggest the presently claimed analytical method using supports having attached oligonucleotides of defined sequences. The two cited references merely provide additional teaching relating to normal dot blot methodologies.

Since the Saiki et al. and the Brigati et al. reference clearly lack an essential element of Applicant's claimed apparatus and method, the 35 U.S.C. 102(b) rejection should be withdrawn and any 35 U.S.C. 103 rejection would clearly be inappropriate.

For the foregoing reasons, it is considered that the rejections on prior art are untenable and should be withdrawn.

No further issues remaining, allowance of this application is respectfully requested. If the Examiner has any comments or proposals for expediting prosecution, he is invited to contact the undersigned at the telephone number below.

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